

#3 0280
0716
OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/772,105 DATE: 02/09/2001
TIME: 11:06:59

Input Set : A:\SEQ LIST 0838.1001-009.txt
Output Set: N:\CRF3\02092001\I772105.raw

ENTERED
See p.5

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3 <110> APPLICANT: Ozelius, Laurie J.
4 Breakefield, Xandra O.
6 <120> TITLE OF INVENTION: TORSIN, TORSIN-RELATED GENES, AND
7 METHODS OF DETECTING NEURONAL DISEASES
9 <130> FILE REFERENCE: 0838.1001009
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/772,105
C--> 12 <141> CURRENT FILING DATE: 2001-01-26
14 <150> PRIOR APPLICATION NUMBER: US 09/218,363
15 <151> PRIOR FILING DATE: 1998-12-22
17 <150> PRIOR APPLICATION NUMBER: US 09/099,454
18 <151> PRIOR FILING DATE: 1998-06-18
20 <150> PRIOR APPLICATION NUMBER: US 60/050,244
21 <151> PRIOR FILING DATE: 1997-06-19
23 <160> NUMBER OF SEQ ID NOS: 90
25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 2597
29 <212> TYPE: DNA
30 <213> ORGANISM: Homo sapien
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (568)...(1563)
36 <221> NAME/KEY: misc_feature /
37 <222> LOCATION: (1)...(2597)
38 <223> OTHER INFORMATION: n = A, T, C or G
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W--> 42 tcttgctctg tctccaggc tggagntgca gtggtgagat ctccgctcac tgcaatctcc 120
W--> 43 gcctcctggg ttcaagngca gttgctcatg tgcagcctc cccagtagct agggctacag 180
44 gtgcctacca ccacaccggc taattttata tttttagtag agacgtggtt tcaccatggt 240
W--> 45 ggtcaggctg gtctcgaact cctgacctca ggtgatccgc ccnccctcagc ctncctcaaaag 300
W--> 46 ggtcgggatt acaggcagga gccaccatnc ctggnaaaaa taacgtccat aaacaaaaaac 360
47 acgtggccaa cagggcggag cagaaccgag ttcccggaag caaacacaggg ctttgtaccg 420
48 aacaaagatg gcggccggcg gcgtcgggag gagggctgcc ctgaagaaag atggcctcgg 480
W--> 49 cgagaggagg aancgggaag cgtgggtctg gcggctgcac cggttcgcgg tcggcgcgag 540
50 aacaagcagg gtggcgcggg tccgggc atg aag ctg ggc cgg gcc gtg ctg ggc 594
51 Met Lys Leu Gly Arg Ala Val Leu Gly
52 1 5
54 ctg ctg ctg ctg gcg ccg tcc gtg gtg cag gcg gtg gag ccc atc agc 642
55 Leu Leu Leu Leu Ala Pro Ser Val Val Gln Ala Val Glu Pro Ile Ser
56 10 15 20 25
58 ctg gga ctg gcc ctg gcc gcc gtc ctc acc gcc tac atc lac ccg cgt 690
59 Leu Gly Leu Ala Leu Ala Gly Val Leu Thr Gly Tyr Ile Tyr Pro Arg
60 30 35 40
62 ctc tac tgc ctc ttc gcc gag tgc tgc ggg cag aag cgg agc ctt agc 738
63 Leu Tyr Cys Leu Phe Ala Glu Cys Cys Gly Gln Lys Arg Ser Leu Ser
64 45 50 55

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66 cgg gag gca ctg cag aag gat ctg gac gac aac ctc ttt gga cag cat 786
67 Arg Glu Ala Leu Gln Lys Asp Leu Asp Asp Asn Leu Phe Gly Gln His
68 60 65 70
70 ctt gca aag aaa atc atc tta aat gcc gtg ttt ggt ttc ata aac aac 834
71 Leu Ala Lys Lys Ile Ile Leu Asn Ala Val Phe Gly Phe Ile Asn Asn
72 75 80 85
74 cca aag ccc aag aaa cct ctc acg ctc tcc ctg cac ggg tgg aca ggc 882
75 Pro Lys Pro Lys Lys Pro Leu Thr Leu Ser Leu His Gly Trp Thr Gly
76 90 95 100 105
78 acc ggc aaa aat ttc gtc agc aag atc atc gca gag aat att tac gag 930
79 Thr Gly Lys Asn Phe Val Ser Lys Ile Ile Ala Glu Asn Ile Tyr Glu
80 110 115 120
82 ggt ggt ctg aac agt gac tat gtc cac ctg ttt gtg gcc aca ttg cac 978
83 Gly Gly Leu Asn Ser Asp Tyr Val His Leu Phe Val Ala Thr Leu His
84 125 130 135
86 ttt cca cat gct tca aac atc acc ttg tac aag gat cag tta cag ttg 1026
87 Phe Pro His Ala Ser Asn Ile Thr Leu Tyr Lys Asp Gln Leu Gln Leu
88 140 145 150
90 tgg att cga ggc aac gtg agt gcc tgt gcg agg tcc atc ttc ata ttt 1074
91 Trp Ile Arg Gly Asn Val Ser Ala Cys Ala Arg Ser Ile Phe Ile Phe
92 155 160 165
94 gat gaa atg gat aag atg cat gca ggc ctc ata gat gcc atc aag cct 1122
95 Asp Glu Met Asp Lys Met His Ala Gly Leu Ile Asp Ala Ile Lys Pro
96 170 175 180 185
98 ttc ctc gac tat tat gac ctg gtg gat ggg gtc tcc tac cag aaa gcc 1170
99 Phe Leu Asp Tyr Tyr Asp Leu Val Asp Gly Val Ser Tyr Gln Lys Ala
100 190 195 200
102 atg ttc ata ttt ctc agc aat gct gga gca gaa agg atc aca gat gtg 1218
103 Met Phe Ile Phe Leu Ser Asn Ala Gly Ala Glu Arg Ile Thr Asp Val
104 205 210 215
106 gct ttg gat ttc tgg agg agt gga aag cag agg gaa gac atc aag ctc 1266
107 Ala Leu Asp Phe Trp Arg Ser Gly Lys Gln Arg Glu Asp Ile Lys Leu
108 220 225 230
110 aaa gac att gaa cac gcg ttg tct gtg tct gtt ttc aat aac aag aac 1314
111 Lys Asp Ile Glu His Ala Leu Ser Val Ser Val Phe Asn Asn Lys Asn
112 235 240 245
113 agt ggc ttc tgg cac agc agc tta att gac cgg aac ctc att gat tat 1362
114 Ser Gly Phe Trp His Ser Ser Leu Ile Asp Arg Asn Leu Ile Asp Tyr
115 250 255 260 265
117 ttt gtt ccc ttc ctc ccc ctg gaa tac aaa cac cta aaa atg tgt atc 1410
118 Phe Val Pro Phe Leu Pro Leu Glu Tyr Lys His Leu Lys Met Cys Ile
119 270 275 280
121 cga gtg gaa atg cag tcc cga ggc tat gaa att gat gaa gac att gta 1458
122 Arg Val Glu Met Gln Ser Arg Gly Tyr Glu Ile Asp Glu Asp Ile Val
123 285 290 295
125 agc aga gtg gct gag gag atg aca ttt ttc ccc aaa gag gag aga gtt 1506
126 Ser Arg Val Ala Glu Glu Met Thr Phe Phe Pro Lys Glu Glu Arg Val
127 300 305 310
129 ttc tca gat aaa ggc tgc aaa acg gtg ttc acc aag tta gat tat tac 1554

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130 Phe Ser Asp Lys Gly Cys Lys Thr Val Phe Thr Lys Leu Asp Tyr Tyr
131      315      320      325
133 tac gat gat/tgacagtcac gattggcagc cggagtcact gctggagatt 1603
134 Tyr Asp Asp
135 330
137 ggaaaagaaa caacactcag tcttccaca ctccacccc cagctccttt ccttggaga 1663
138 ggaatccagt gaattgttct gtttgatgtg acaggaattc tccctggcat tgtttccacc 1723
139 ccttggtgcc tgcaggccac ccagggaacca cgggcgagga cgtgaaacct cccgaacacg 1783
140 cacagaagga aggagccagc tcccagccca ctcatcgag ggtcatgat tttttacaaa 1843
141 ttatgtttta attccaagtg tttctgtttc aaggaaggat gaataagttt tattgaaaat 1903
142 gtggtaactt tattttaaatt gatttttaac attatgagag actgctcaga ttctaagttg 1963
143 ttggccttgt gtgtgtgttt ttttttaagt tctcatcatt attacataga ctgtgaagta 2023
144 tctttactgg aaatgagccc aagcacacat gcatggcatt tgttcctgaa caggagggca 2083
145 tccctgggga tgtggctgga gcatgagcca gctctgtccc aggatggtcc cagcggatgc 2143
146 tgcagggggc agtgaagtgt ttaggtgaag gacaagtagg taagaggacg ccttcaggca 2203
147 ccacagataa gctgaaaca gctctccaa qggttttcac cttagcaaca atgggagctg 2263
148 tgggagtgat tttggccaca ctgtcaacat ttgttagaac cagtcttttg aaagaaaagt 2323
149 atttccaact tgtcaactgc cagtcactcc gttttgcaaa aggtggccct tcaactgtcca 2383
150 ttccaaatag ccacacagtg ctctctgtcg gattctaaat tatgtgaatt ttgccatatt 2443
151 aaatcttctt catttatact attatttgtt acgttcaatc agaatecccg aaacctccta 2503
152 taaagcttag ctgccccttc tgaggatgct gagaacggtg tctttcttta taaatgcaaa 2563
153 tggctaccgt tttacaataa aattttgcat gtgc 2597
155 <210> SEQ ID NO: 2
156 <211> LENGTH: 332
157 <212> TYPE: PRT
158 <213> ORGANISM: Homo sapien
160 <400> SEQUENCE: 2
161 Met Lys Leu Gly Arg Ala Val Leu Gly Leu Leu Leu Leu Ala Pro Ser
162 1 5 10 15
163 Val Val Gln Ala Val Glu Pro Ile Ser Leu Gly Leu Ala Leu Ala Gly
164 20 25 30
165 Val Leu Thr Gly Tyr Ile Tyr Pro Arg Leu Tyr Cys Leu Phe Ala Glu
166 35 40 45
167 Cys Cys Gly Gln Lys Arg Ser Leu Ser Arg Glu Ala Leu Gln Lys Asp
168 50 55 60
169 Leu Asp Asp Asn Leu Phe Gly Gln His Leu Ala Lys Lys Ile Ile Leu
170 65 70 75 80
171 Asn Ala Val Phe Gly Phe Ile Asn Asn Pro Lys Pro Lys Lys Pro Leu
172 85 90 95
173 Thr Leu Ser Leu His Gly Trp Thr Gly Thr Gly Lys Asn Phe Val Ser
174 100 105 110
175 Lys Ile Ile Ala Glu Asn Ile Tyr Glu Gly Gly Leu Asn Ser Asp Tyr
176 115 120 125
177 Val His Leu Phe Val Ala Thr Leu His Phe Pro His Ala Ser Asn Ile
178 130 135 140
179 Thr Leu Tyr Lys Asp Gln Leu Gln Leu Trp Ile Arg Gly Asn Val Ser
180 145 150 155 160
181 Ala Cys Ala Arg Ser Ile Phe Ile Phe Asp Glu Met Asp Lys Met His
182 165 170 175

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183 Ala Gly Leu Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Asp Leu
184          180          185          190
185 Val Asp Gly Val Ser Tyr Gln Lys Ala Met Phe Ile Phe Leu Ser Asn
186          195          200          205
187 Ala Gly Ala Glu Arg Ile Thr Asp Val Ala Leu Asp Phe Trp Arg Ser
188          210          215          220
189 Gly Lys Gln Arg Glu Asp Ile Lys Leu Lys Asp Ile Glu His Ala Leu
190 225          230          235          240
191 Ser Val Ser Val Phe Asn Asn Lys Asn Ser Gly Phe Trp His Ser Ser
192          245          250          255
193 Leu Ile Asp Arg Asn Leu Ile Asp Tyr Phe Val Pro Phe Leu Pro Leu
194          260          265          270
195 Glu Tyr Lys His Leu Lys Met Cys Ile Arg Val Glu Met Gln Ser Arg
196          275          280          285
197 Gly Tyr Glu Ile Asp Glu Asp Ile Val Ser Arg Val Ala Glu Glu Met
198          290          295          300
199 Thr Phe Phe Pro Lys Glu Arg Val Phe Ser Asp Lys Gly Cys Lys
200 305          310          315          320
201 Thr Val Phe Thr Lys Leu Asp Tyr Tyr Tyr Asp Asp
202          325          330
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206 <211> LENGTH: 3568
207 <212> TYPE: DNA
208 <213> ORGANISM: Homo sapien
210 <220> FEATURE:
211 <221> NAME/KEY: CDS
212 <222> LOCATION: (994)...(1863)
214 <221> NAME/KEY: misc_feature
215 <222> LOCATION: (1)...(3568) /
216 <223> OTHER INFORMATION: n = A,T,C or G
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220 ccagcctgag acagtttcgc tcttgtcgcc caggctggag tgcagtggca cgatctcggc 120
221 taactgcaac ctccgcctcc tgggttcaa agattctcct gcctcaacct ccgagtagct 180
W--> 222 gggattacag gcgyscgccr csmcrsccag cntttttttt tttttttgag acagtttcgc 240
W--> 223 tcttgtcgcc aggetggagt gcagtgnnng anctcggtta actgcaactc cgctctctgg 300
W--> 224 gttaagaga ttctnctgcc tcaactcccc agtagctggg attataggng nccgcnacca 360
225 caccatctaa ttttttggat ttttagtaga gacgggggtt cgcacgttga gcaggctggg 420
226 ctggaactcc tgacatcagg tgatccgccc gattcagctt cccaaagtgc tgggattaca 480
227 ggcgtgagca cggcgcccg ccaaaaaaaaa aatatttttt tttttttttt agatattttt 540
228 tcaactcttg tgeccaggct ggagtgaat ggcgatgatc cggctcgccc tcccaaagtc 600
W--> 229 ctgggattac aggcgtgaca ccgngcccg sccgaaaaaa twtttttaaa agaaaaagg 660
230 aaacaaamag tctctacac cttegrccac tcccaagaac gatggsacss cctcctctyc 720
W--> 231 gnccctmacc aacctggcc gnccnaagg gagtggggcg ggtctgcggg gcggaagtga 780
232 cgsacgagag gaagtccgtc ctgcgcttgg ccgcggggcg cctggctcag tggcttctgc 840
233 gggcttcgag gagcgggatg ttgcgggctg ggtggctccg ggcgcggcgg cgctggcgct 900
234 gctgctggcg gcccgagtgg tggcgagtt cgagcccatc accgtgggcc tagccatcgg 960
235 gcaggtcggc catcacccgc tacctgtcct aca tatg aca tct act gcc cgt tcg 1014
236          Met Thr Ser Thr Ala Arg Ser

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237
239 ccg agt gct gcc ggc gag gag cgg ccg ctc aac gct tgg gct ctc aag 1062
240 Pro Ser Ala Ala Gly Glu Glu Arg Pro Leu Asn Ala Ser Ala Leu Lys
241 10 15 20
243 ctg gat ttg gag gag aag ctg ttt gga cag cat cta gcc acg gaa gtg 1110
244 Leu Asp Leu Glu Glu Lys Leu Phe Gly Gln His Leu Ala Thr Glu Val
245 25 30 35
247 att ttc aag gcg ctg act ggc ttc agg aac aac aaa aat ccc aag aaa 1158
248 Ile Phe Lys Ala Leu Thr Gly Phe Arg Asn Asn Lys Asn Pro Lys Lys
249 40 45 50 55
251 cca ctg acc ctt tcc tta cac ggc tgg gct ggc aca ggc aag aat ttt 1206
252 Pro Leu Thr Leu Ser Leu His Gly Trp Ala Gly Thr Gly Lys Asn Phe
253 60 65 70
255 gtc agt caa att gtg gct gaa aat ctt cac cca aaa ggt ctg aag agt 1254
256 Val Ser Gln Ile Val Ala Glu Asn Leu His Pro Lys Gly Leu Lys Ser
257 75 80 85
259 aac ttt gtc cac ctg ttt gta tgg act ctg cac ttc cct cat gag cag 1302
260 Asn Phe Val His Leu Phe Val Ser Thr Leu His Phe Pro His Glu Gln
261 90 95 100
263 aag ata aaa ctg tac cag gac cag tta cag aag tgg atc cgc ggt aat 1350
264 Lys Ile Lys Leu Tyr Gln Asp Gln Leu Gln Lys Trp Ile Arg Gly Asn
265 105 110 115
267 gtg agt gca tgt gcg aac tct gtt ttc ata ttt gac gag atg gat aaa 1398
268 Val Ser Ala Cys Ala Asn Ser Val Phe Ile Phe Asp Glu Met Asp Lys
269 120 125 130 135
271 ttg cac ccc ggg atc att gac gca atc aag ccg ttt cta gac tac tac 1446
272 Leu His Pro Gly Ile Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr
273 140 145 150
275 gag cag gtt gac gga gtg tct tac cgc aaa gcc atc ttc atc ttt ctc 1494
276 Glu Gln Val Asp Gly Val Ser Tyr Arg Lys Ala Ile Phe Ile Phe Leu
277 155 160 165
279 agc aat gca ggc ggg gac ctt ata act aag acg gct ctt gac ttt tgg 1542
280 Ser Asn Ala Gly Gly Asp Leu Ile Thr Lys Thr Ala Leu Asp Phe Trp
281 170 175 180
283 cgg gcc gga aga aag agg gaa gac att cag ctg aag gac ctg gaa cct 1590
284 Arg Ala Gly Arg Lys Arg Glu Asp Ile Gln Leu Lys Asp Leu Glu Pro
285 185 190 195
287 gta ctg tct gtc gga gtc ttc aat aat aaa cac agt ggc ctg tgg cac 1638
288 Val Leu Ser Val Gly Val Phe Asn Asn Lys His Ser Gly Leu Trp His
289 200 205 210 215
291 agt gga ctg atc gac aaa aac ctc att gat tac ttt atc ccc ttc ctg 1686
292 Ser Gly Leu Ile Asp Lys Asn Leu Ile Asp Tyr Phe Ile Pro Phe Leu
293 220 225 230
295 cct ttg gag tac aga cat gtg aaa atg tgt gtg agg gcc gag atg agg 1734
296 Pro Leu Glu Tyr Arg His Val Lys Met Cys Val Arg Ala Glu Met Arg
297 235 240 245
299 gcc cgt ggt tct gcc ata gat gaa gac att gtc aca aga gtg gca gag 1782
300 Ala Arg Gly Ser Ala Ile Asp Glu Asp Ile Val Thr Arg Val Ala Glu
301 250 255 260

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← F.Y.I.

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/772,105

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Input Set : A:\SEQ LIST 0838.1001-009.txt

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:41 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:42 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:43 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:45 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:46 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:49 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:222 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:223 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:224 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:229 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:231 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:779 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:907 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:923 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1056 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1151 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:1466 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48
L:1484 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49
L:1486 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49
L:1502 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50
L:1503 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50
L:1505 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50
L:1506 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50
L:1507 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50
L:1525 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
L:1526 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
L:1527 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
L:1528 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
L:1529 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
L:1566 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53
L:1568 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53
L:1603 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55
L:1604 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55
L:1621 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56
L:1622 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56
L:1659 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57
L:1675 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58
L:1676 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58
L:1678 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58
L:1696 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59
L:1735 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61
L:1736 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61
L:1751 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62
L:1753 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62
L:1755 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62
L:1756 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62

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L:1775 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63
L:1807 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:65
L:1827 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:2082 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:88